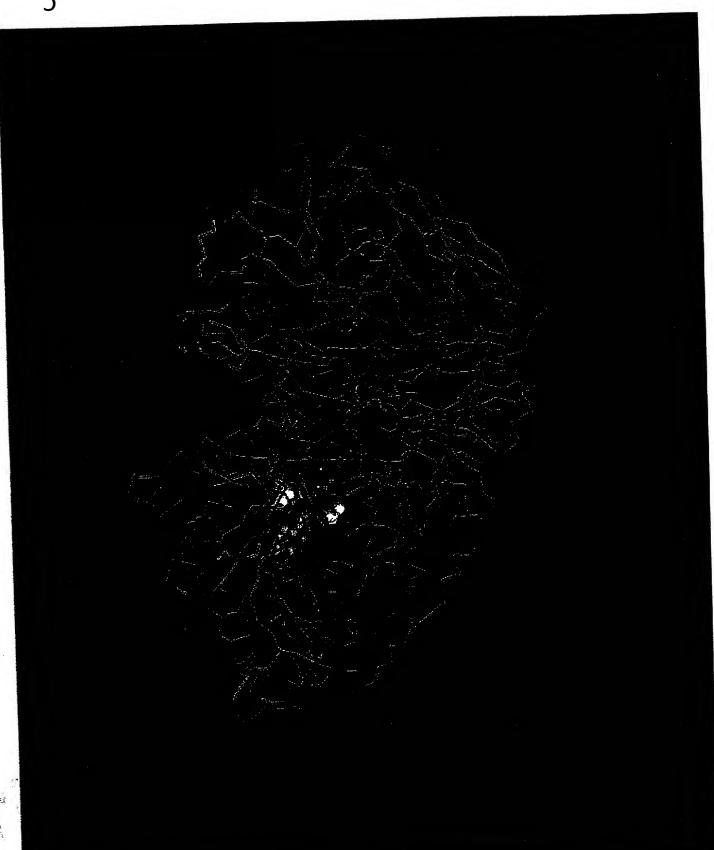




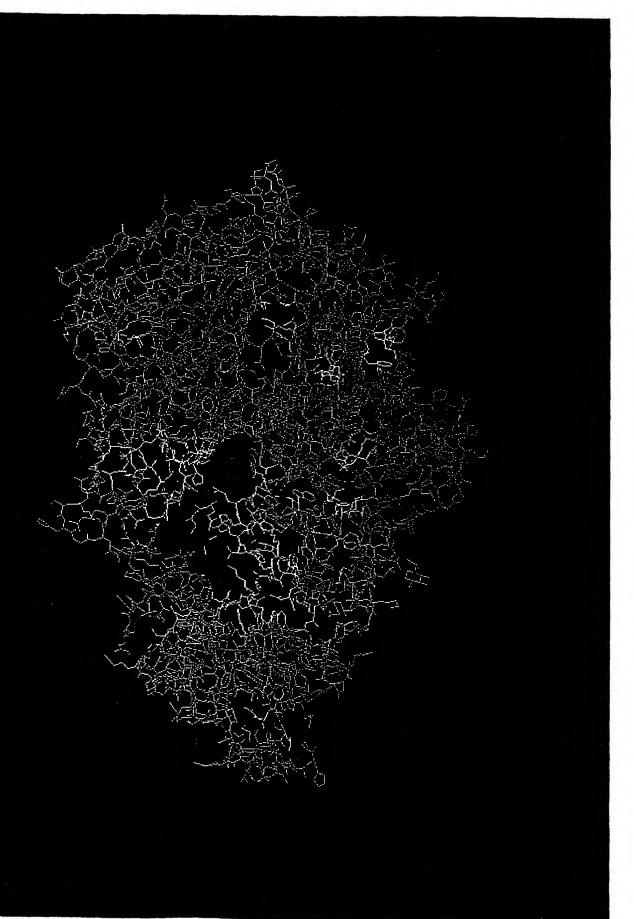
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Title: MANNOSIDASE STRUCTURES
Serial No.: 09/960226
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Fig.3

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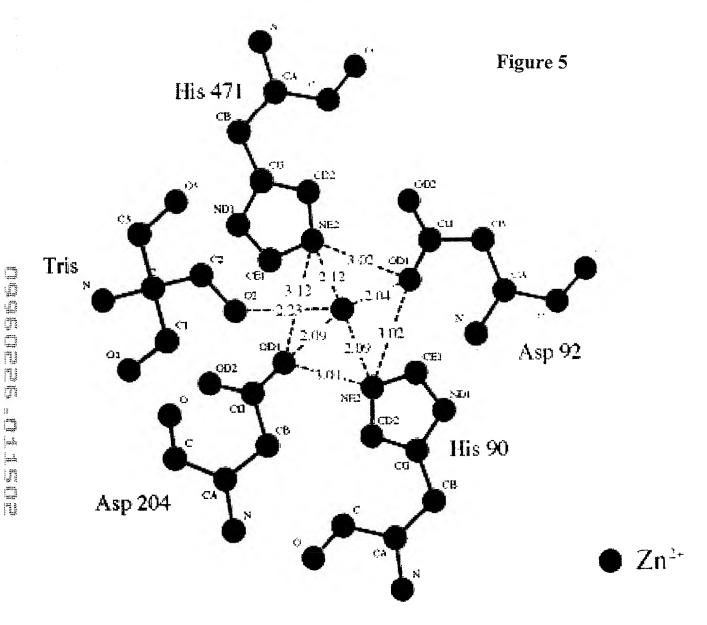


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pMT/BiP-N-HIS-dGMII [851 to 4042] -> 1-phase Translation

DNA sequence

6642 b.p. TCGCGCGTTTCG ... AGGCCCTTTCGT circular

Figure 6

N-HIS added to pMTV5HisA (b/t BglII/EcoRI) for drosophilla expression of tagged proteins. Add drosophila dGMII from clone D11 (shortened 3') DAK/Tara 15-3-99

851/1 atg AAG TTA TGC	- ama m	ra corc		CTC.	CTC	881/		بلغلت	ccc	cm	***	~~	~~	=~=	tat	911/21		t cat	cat	cat	cac	003	~22	مرتمان
M K L C																								
941/31						971/	41									1001/5	51							
gac gat cca ata																								
	R P	P	L	K	V			s	P	R	P	G	Q	С	Q	D V 1091/8		Q	D	V	P	N	V	D
1031/61 gta cag atg ctg	man c	a tac	crat	cac	ato	1061		aact	oac	ata	gat	OOA	aac	ata	taa			e tac	aac	att	aac	tac	gat	cca
V Q M L																								P
1121/91							/101									1181/1								
ctg aag tac aac																								
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N M L I 1661/271	Q R	T	H	Y					E	L	A	Q	Ω.	R		L E 1721/2		L	W	R	Q	I	W	D
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N K G D																H T								
1751/301						1781										1811/3								
tgt cag ttc gat																								
C Q F D	r K	R	M	G		r 1871			5	C	P	M	r.	V	P	P K 1901/3		1	5	D	Q	N	V	A
gca ege tea gat	ctq c	a att	gat	саσ					gcc	gag	ctg	tat	ege	aca	aac			att	CCT	ttq	qat	gac	gac	ttc
ARSD		v		Q												ν L			P				_	F
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2111/421 gac ttt ttc aca D F F T 2201/451	tac go Y A	L c gat D	Q cga R	E tcg S	Y gat D	F 2141 aac N 2231	D /431 tat Y /461	A tgg W	V agt S	H ggc G	Q tac Y	A tac Y	E aca T	R tec S	A ege R	G Q 2171/4 ccg tz P Y 2261/4	A 141 it ca H 171	E taag K	F cgc R	P atg M	T gac D	L ege R	S gtc V	G ctg L
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta	tac go Y A	L c gat D a gca	Q cga R gaa	E teg S atg	Y gat D ctt	F 2141 aac N 2231 tec	D /431 tat Y /461 gec	A tgg W tgg	V agt S cac	H ggc G tec	Q tac Y tgg	A tac Y gac	e aca T ggt	R tec S atg	A ege R gee	G Q 2171/4 ccg tz P Y 2261/4 cgc at	A 141 it ca H 171 ic ga	E taag K ggaa	F cgc R cgt	P atg M ctg	T gac D gag	L ege R cag	S gtc V gcc	G ctg L cgc
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V	tac go Y A	L c gat D a gca	Q cga R gaa	E teg S atg	Y gat D ett L	F 2141 aac N 2231 tec S	D /431 tat Y /461 gec A	A tgg W tgg K	V agt S cac	H ggc G tec	Q tac Y tgg	A tac Y gac	e aca T ggt	R tec S atg	A ege R gee A	G Q 2171/4 ccg tz P Y 2261/4 cgc at R I	A 141 it ca H 171 cc ga	E taag K ggaa	F cgc R cgt	P atg M ctg	T gac D gag	L ege R cag	S gtc V gcc	G ctg L cgc
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta	tac go Y A cgt go R A	L c gat D ca gca A	Q cga R gaa E	E teg S atg M	Y gat D ett L	F 2141 aac N 2231 tec S 2321	D /431 tat Y /461 gcc A /491	A tgg W tgg W	V agt S cac H	H ggc G tec S	Q tac Y tgg W	tac Y gac D	E aca T ggt G	R tec S atg M	A ege R gee A	G Q 2171/4 ccg tz P Y 2261/4 cgc at R I 2351/5	A 141 It ca If 171 IC ga E	E taag K ggaa E	F Cgc R cgt R	p atg M ctg L	T gac D gag E	L cgc R cag Q	S gtc V gcc A	G ctg L cgc R
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S	tac go Y A cgt go R A	L gat D a gca A c cag	Q cga R gaa E	tcg s atg M	y gat D ctt L gac D	F 2141 aac N 2231 tec S 2321 ggt G	D /431 tat Y /461 gec A /491 ata	tgg W tgg W act	V agt S cac H	H ggc G tec S aca	Q tac Y tgg W	tac Y gac D	e aca T ggt G	R tec S atg M	A cgc R gcc A gta V	G Q 2171/4 ccg tz P Y 2261/4 cgc at R I 2351/5 gtc gt	A 141 171 172 160 160 160 170 170 170 170 170 170 170 170 170 17	E taag K ggaa E ctac	cgc R cgt R	atg M ctg L caa	T gac D gag E cgc	L cgc R cag Q	S gtc V gcc A cag	G ctg L cgc R
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511	tac go Y A cgt go R A ttg ti L F	L gat D ca gca A ce cag	Q cga R gaa E cac H	teg s atg M cac H	y gat D ett L gac D	F 2141 aac N 2231 tec S 2321 ggt G 2411	D /431 tat Y /461 gec A /491 ata I /521	tgg W tgg W act	V agt S cac H ggc G	H ggc G tec S aca	Q tac Y tgg W gca A	tac Y gac D aaa	E aca T ggt G acg T	R tec S atg M cac H	A cgc R gcc A gta V	G Q 2171/4 ccg tz P Y 2261/4 cgc at R I 2351/5 gtc gt V V 2441/5	A 141 at ca 171 ac ga E 501 ac ga D 531	E taag K ggaa E ctac	F cgc R cgt R	atg M ctg L caa	T gac D gag E cgc R	L egc R cag Q atg M	gtc V gcc A cag Q	G ctg L cgc R gaa E
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc	tac go Y A cgt go R A ttg tt L F	L cc gat D ca gca A cc cag Q	Q cga R gaa E cac H	teg s atg M cac H	y gat D ctt L gac D	F 2141 aac N 2231 tec S 2321 ggt G 2411 cag	D /431 tat Y /461 gcc A /491 ata I /521 tcg	tgg W tgg W act T	V agt S cac H ggc G	H ggc G tec S aca T	Q tac Y tgg W gca A	tac Y gac D aaa K	E aca T ggt G acg T	R tec S atg M cac H	A cgc R gcc A gta V	G Q 2171/4 ccg tz P Y 2261/4 cgc at R I 2351/5 gtc gt V V 2441/5 tcc at	A 141 1t ca 171 1c ga 160 160 160 160 160 160 160 160 160 160	E taag gaa E taa	cgc R cgt R gag	atg M ctg L caa Q	gac D gag E cgc R	Cgc R cag Q atg M	gtc V gcc A cag Q	G ctg L cgc R gaa E
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511	tac go Y A cgt go R A ttg tt L F	L gat D ca gca A ce cag	Q cga R gaa E cac H	teg s atg M cac H	y gat D ctt L gac D caa Q	F 2141 aac N 2231 tec S 2321 ggt G 2411	D /431 tat Y /461 gcc A /491 ata I /521 tcg S	tgg W tgg W act T	V agt S cac H ggc G	H ggc G tec S aca T	Q tac Y tgg W gca A	tac Y gac D aaa K	E aca T ggt G acg T	R tec S atg M cac H	A cgc R gcc A gta V	G Q 2171/4 ccg tz P Y 2261/4 cgc at R I 2351/5 gtc gt V V 2441/5	A 141 15 ca 171 16 ga 1601 16 ga 161 16 ga 1631 16 ta	E taag gaa E taa	F cgc R cgt R	atg M ctg L caa Q	gac D gag E cgc R	Cgc R cag Q atg M	gtc V gcc A cag Q	G ctg L cgc R gaa E
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc	tac go Y A ogt go R A ttg to L F tgt co C Q	L cc gat D ca gca A cc cag Q ca atg	Q cga R gaa E cac H gta V cgc	teg s atg M cac H atg K	y gat D ctt L gac D caa Q cca	F 2141 aac N 2231 tec S 2321 ggt G 2411 cag Q 2501 gga	D /431 tat Y /461 gcc A /491 ata I /521 tcg S /551	tgg W tgg W act T gtc V	V agt S cac H ggc G tac Y	H ggc G tec S aca T cga R	Q tac Y tgg W gca A ttg L	tac Y gac D aaa K ctg L	E aca T ggt G acg T aca T cga	tcc S atg M cac H aag K	A cgc R gcc A gta V ccc P acc	G Q 2171/4 cog tz P Y 2261/4 cgc at R I 2351/5 gtc gt V V 2441/5 tcc at S I 2531/5 ata at	A 141 at ca 171 ac ga 501 ac ga 1531 ac ta 1561 ta ct	E taag K g gaa E taac Y c agt S	F cgc R cgt R cgg E ccg P gag	P atg M ctg L caa Q gac D	T gac D gag E cgc R ttc F ata	L ege R cag Q atg M agt s	gtc V gcc A cag Q ttc F	ctg L cgc R gaa E tcg s
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L	tac go Y A ogt go R A ttg to L F tgt co C Q	L cc gat D ca gca A cc cag Q ca atg	Q cga R gaa E cac H gta V cgc	teg s atg M cac H atg K	y gat D ctt L gac D caa Q cca	F 2141 aac N 2231 tec S 2321 ggt G 2411 cag Q 2501 gga G	D /431 tat Y /461 gec A /491 ata I /521 teg S /551 tet S	tgg W tgg W act T gtc V ggt	V agt S cac H ggc G tac Y	H ggc G tec S aca T cga R	Q tac Y tgg W gca A ttg L	tac Y gac D aaa K ctg L	E aca T ggt G acg T aca T cga	tcc S atg M cac H aag K	A cgc R gcc A gta V ccc P acc	G Q 2171/4 cog tz P Y 2261/4 cgc at R I 2351/5 gtc gt V V 2441/5 tcc at S I 2531/5 ata at I I	A 141 at ca H 171 ac ga 501 ac ga 1531 ac ta 1561 ac ta	E taag K g gaa E taac Y c agt S	F cgc R cgt R cgg E ccg P gag	P atg M ctg L caa Q gac D	T gac D gag E cgc R ttc F ata	L ege R cag Q atg M agt s	gtc V gcc A cag Q ttc F	ctg L cgc R gaa E tcg s
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2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601	tac gg Y A cgt gg R A ttg tc L F tgt cc C Q gac gac D D atg cc M H	L c gat D c gag a gca A c cag Q ua atg u tec S uc aac	Q cga R gaa E cac H gta V cgc R acc T	teg s atg M cac H atg M tgg W	Y gat D ctt L gac D caa Q cca P ccc	F 2141 aac N 2231 tec S 2321 ggt C 2411 cag Q 2501 g G 2591 cac H 2681	D /431 tat y /461 gcc A /491 ata I /521 tcg S /551 tct S /581 tgg W /611	tgg W tgg W act T gtc V ggt G	V agt S cac H ggc G tac Y gtg V gag E	H gggc G tecc S aca T cga R gag E cag Q	Q tac Y tgg W gca A ttg L gac D ctg L	tac y gac D aaaa K ctg L agt s	E aca T ggt G acg T aca T cga R gac	R tec S atg M cac H aag K acc T ttt	A cgc R gcc A gta V ccc P acc T tat Y	G Q 2171/4 2171/4 P Y 2261/4 egc at R I 2351/5 gtc gt y V 2441/5 tcc at S I 2531/5 ata at I I 2621/5 gta tc V S 2711/6	A 141 it ca 171 ic ga 601 ic ga 161 ic ta 161 ic ta 163 ic ta 27 ica t 163 i	E taas K g gaa E taas Y c agt S g ggo G t cog	F Cgc R Cgt R Gag F Ccg F Ccg F Cttt F	P atg M ctg L caa Q gac D gat V	T gac D gag E cgc R ttc F ata I agc S	L egc R cag Q atg M agt S etg L gtt V	S gtc V gcc A cag Q ttc F ccc P acc T	G ctg L cgc R gaa E tcg s tcc S
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat	tac gray A cgt gar gar cc Q gar gar gar cc M H cc gg gar gar gar gar gar gar gar gar gar	L c gat D c gag a gca A c cag Q ua atg M ac tec S ac aac N cg gag	Q cga R gaa E cac H gta V cgc R acc T gct	tcg S atg M cac H atg M tgg W ctg L cag	y gat D ctt L gac D caa Q cca P ccc P gtg	F 2141 aac N 2231 tec S 2321 ggt Cag Q 2501 gga G 2591 Cag L 2591 Ca H 2681 tec	D /431 tat Y /461 gcc A /491 ata I /521 tcg S /551 tct S /581 tg /611 ccg /611	A tgg W tgg W act T gtc Cgg R gtg	v agt s cac H ggc tac Y gtg v tag t	H gggc G tec S aca T cga R gag C aga G aga G aga A aga	Q tac Y tag W gca A ttg gac D ctg L tgg	tac Y gac D aaaa K ctg L agt S gtg V cac	E aca T ggt aca T cga R gac D cac	R tec S atg M cac H aaag K acc T ttt F	A cgc R gcc A gta V ccc P acc T tat Y aca	G Q 2171/4 ccg tz P Y 2261/4 cgc at R I 2351/5 gtc gt V Y 2441/5 tcc at S I 2531/5 ata at I I 2621/5 gta tc V S 2711/4 cctc ac	A 141 at ca H 171 ac ga E 501 ac ta Y 561 ac ta L 591 ac aa aa	E t aag K gaa E t tac Y c agt S gag G g g g g g g g g g g g g	F CGC R Cgt R Gag F CGG F Gag F CGG F Gag F CGG	atg M ctg L caa Q gac D gat D	T gac D gag E cogc R ttc F ata I agc S cca	L cgc R cag Q atg M agt S ctg L gtt V caa	gtc V gcc A cag Q ttc F cec P	G ctg L cgc R gaa E tcg S tcc S gac D
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat L A N N	tac gray A cgt gar gar cc Q gar gar gar cc M H cc gg gar gar gar gar gar gar gar gar gar	L c gat D c gag a gca A c cag Q ua atg M ac tec S ac aac N cg gag	Q cga R gaa E cac H gta V cgc R acc T gct	tcg S atg M cac H atg M tgg W ctg L cag	y gat D ctt L gac D caa Q cca P ccc P gtg	F 2141 aac N 2231 tee S 2321 ggt G 2411 ca G 2 2501 gga G 2591 cac H 2681 tee S	D /431 tat Y /461 gcc A /491 ata I /521 tcg S /551 tct S /581 tct S /581 ccg P	A tgg W tgg W act T gtc Cgg G G G G G G G G G G G G G G G G G G	v agt s cac H ggc tac Y gtg v tag t	H gggc G tec S aca T cga R gag C aga G aga G aga A aga	Q tac Y tag W gca A ttg gac D ctg L tgg	tac Y gac D aaaa K ctg L agt S gtg V cac	E aca T ggt aca T cga R gac D cac	R tec S atg M cac H aaag K acc T ttt F	A cgc R gcc A gta V ccc P acc T tat Y aca T	G Q Q 2171/4 coc tz P Y 2261/4 coc at R I 2351/5 gtc gt V V Y 2441/5 tcc at S I I I I 2621/5 gta tc V S 2711/6 ctc ac L T	A 141 at ca 171 ac ga E 501 ac ga B 501 ac ta	E t aag K gaa E t tac Y c agt S gag G g g g g g g g g g g g g	F CGC R Cgt R Gag F CGG F Gag F CGG F Gag F CGG	atg M ctg L caa Q gac D gat D	T gac D gag E cogc R ttc F ata I agc S cca	L cgc R cag Q atg M agt S ctg L gtt V caa	gtc V gcc A cag Q ttc F cec P	G ctg L cgc R gaa E tcg S tcc S gac D
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat L A N N 2741/631 acc acc aag tac	tac gg Y A cgt gg R A ttg ti L F tgt cc C Q gac ga D D atg cc M H ccg gg P V	L c gat a gca A c cag Q ua atg u tec S ac aac N c gag E	Q cga R gaa E cac H gta V cgc R acc T gct A ttc	E tcg S atg M cac H atg W ctg Ctg L cag Q aag	y gat D ctt L gac D caa Q cca P ccc P gtg V gct	F 2141 aac N 2231 ttee S 2321 tggt G 2411 cag Q 2501 gga G 2591 cac H 2681 ttee S 2771 cgg	D /431 tat y /461 gec A /491 ata i /521 teg S /551 tet S /561 teg W /611 eeg P /641	A tgg W tgg W tgg W act G G G G G G G G G G G G G G G G G G G	V agt S cac R ggc G tac Y gtg V gag E tgg	H ggc G tcc S aca T cga R gag E cag Q agc s atg	Q tac Y tgg W gca A ttg C C C C C C C C C C C C C C C C C C	tac Y gac D aaa K ctg L agt S gtg V cac H ttg	E aca T gggt acg T aca T cga R cac H gcc	R tee S atg M cac H aaag K aeee T ttt F gae D aee	A cgc R gcc A gta V ccc P acc T tat Y aca T tac	G Q 2171/4 2171/4 2261/4 2261/4 2261/4 2351/5 2441/5 2441/5 2531/5 2441/5	A 141 cat	E t aasg K grad E t aasg grad E t ac Y c agt grad G G G G T c catcaca T	F CGC R CGT R GAG E GGG P GAG E CCC P GAG E CCC P GAG E CCC P GAG E CCC P CGG E CCC P CCC P CGG E CCC P CCC	patg Mctg Lcaa Qgac Dgac Dgat Vcac H	T gac D gag gag E cgc R ttc F ata I agc S cca P tcc	L cgc R cag Q atg M agt S ctg L gtt V caa Q aag	S gtc V gcc A cag Q ttc F ccc P acc T ggc C Cca	G ctg L cgc R gaa E tcg S tcc S gac D tcc S gag
2111/421 gac ttt tc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat L A N 2741/631 acc acc aag tac T T K Y	tac gg Y A cgt gg R A ttg ti L F tgt cc C Q gac ga D D atg cc M H ccg gg P V	L c gat a gca A c cag Q ua atg u tec S ac aac N c gag E	Q cga R gaa E cac H gta V cgc R acc T gct A ttc	E tcg S atg M cac H atg W ctg Ctg L cag Q aag	y gat D ctt L gac D caa Q cca P ccc P gtg V gct	F 2141 aac N 2231 ttee S 2321 cag Q 2501 gga G 2591 cac H 2681 ttee S 2771 cgg R	D /431 tat y /461 gec A /491 ata I /521 teg S /551 tet S S /551 teg W /611 eeg P /641 gtg V	A ttgg W ttgg W act T gtc V ggt Ccgg R gtg V ccg	V agt S cac R ggc G tac Y gtg V gag E tgg	H ggc G tcc S aca T cga R gag E cag Q agc s atg	Q tac Y tgg W gca A ttg Cac D ctg L tgg W ggc	tac Y gac D aaa K ctg L agt S gtg V cac H ttg	E aca T gggt acg T aca T cga R cac H gcc	R tee S atg M cac H aaag K aeee T ttt F gae D aee	A cgc R gcc A gta V ccc P acc T tat Y aca T tac	G Q 2171/4 2171/4 2261/4 2261/4 2261/4 2351/5 251/5 2521/5 2521/5 2521/5 2521/5 2521/5 2521/5 2521/5 2521/5 2521/6	A 141 at cas H 171 ac ga E 501 ac ta L 591 ac S 521 ac ac T T 555 a ac T	E t aasg K grad E t aasg grad E t ac Y c agt grad G G G G T c catcaca T	F CGC R CGT R GAG E GGG P GAG E CCC P GAG E CCC P GAG E CCC P GAG E CCC P CGG E CCC P CCC P CGG E CCC P CCC	patg Mctg Lcaa Qgac Dgac Dgat Vcac H	T gac D gag gag E cgc R ttc F ata I agc S cca P tcc	L cgc R cag Q atg M agt S ctg L gtt V caa Q aag	S gtc V gcc A cag Q ttc F ccc P acc T ggc C Cca	G ctg L cgc R gaa E tcg S tcc S gac D tcc S gag
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat L A N 2741/631 acc acc aag tac T T K Y 2831/661	tac gg Y A cgt gg R A ttg tc L F tgt cc C Q gac gc D D atg cc M H ccg gg P V cgc at	L gat grand A A A A A A A A A A A A A A A A A A A	Q cga R gaa E cac H gta V cgc R acc T gct A ttc F	tcg s atg M cac H atg W ctg L cag Q aaag K	gat D ctt L gac D caa Q cca P ccc P gtg V	F 2141 aac N 2231 tee S 2321 gg C 2411 cag Q 2501 gga G 2591 tee S 2771 cgg R R 2861	D /431 tat /461 gcc A /491 ata i./521 tcg S /551 tct S /581 tgg W /611 gtg V /671	A ttgg W ttgg W act T gtc Cgg R gtg V ccg	v agt s cac H ggc G tac Y gtg V gag E tgg W ccc P	H ggc G tec S aca T cga R gag C S atg	Q tac Y tgg W gca A ttg gac D ctg L tgg W ggc G	A tac Y gac D aaaa K ctg L agt S gtg V cac H ttg L	E aca T ggt aca T cga R gac H gcc A	R teccs atg M cac H aag K acc T ttt F gac D acc	A cgc R gcc A gta v ccc P acc T tat Y aca T tac Y	G Q 2171/4 2171/4 2261/4 2261/4 2441/5 251	A 141 ca 141 ca 171 cc ga E 501 cc ga cc ga cc ga cc ta 1561 cc ta 1561 cc a	E t aag K ggaag E t aag E c taa Y c ag G G G G G G G G G G G G G G G G G G G	F CGC R Sagage F E ttt F atc I tcc S	P atg M ctg L caa Q gac D gat D cac H gat	T gac D gag E cogc R ttc F ata I .agc S cca P tcc S	L cgc R cag Q atg M agt s ctg L gtt V caa Q aagg K	gtc V gcc A cag Q ttc F ecc P acc T ggc G	G ctg L cgc R gaa E tcg S tcc S gac D tcc S gag E
2111/421 gac ttt tc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat L A N 2741/631 acc acc aag tac T T K Y	tac gg Y A cgt gg R A ttg tc L F tgt cg C Q gac gg D D atg cc M H ccg gg P V cgc ac R I gca tc	L gat p gag gag gag gag gag gag gag gag gag g	Q cga R gaa E cac H gta V cgc R acc T gct A ttc F ctc	tcg s atg M cac H atg W ctg L cag Q aaag K ttg	y gat D cett L gac D caa Q cca P ccc P gtg V gct A ctc	F 2141 an N 2231 tec S 2321 ggt G 2411 ca Q Q 2501 gga G 2591 cac H 2681 te S 2771 cgg R 2691 cgt cgt cgt	D /431 tat /4461 gcc A /491 ata ./521 tcg S ./551 tct S S ./581 tgg W /611 ccg P /641 gtg V /671 aaa	A ttgg W ttgg W act T gtc G G G G G G G G G G G G G G G G G G G	v agt S cac R ggc G tac Y gtg V ccc P ccg	H ggc G tec S aca T cga R ggag E cag Q agc S atg M act	Q tac Y tgg W gca A ttg L gac D ctg L tgg W ggc ttgg t	A tac Y gac D aaaa K ctg L agt S gtg V cac H ttg L	E aca T ggt G acg T aca T cga R G acg D cac H gcc A cca	R tecc S atg M Cac H aaag K acc T ttt F gac T ttt ttg	A cgc R gcc A gta V ccc P acc T tat Y aca T tac Y ggc	G Q 2171/4 2171/4 2261/4 2261/4 2441/5 251	A 141 at cas H 171 at cas E 171	E aagg gaage E c tac Y S G G G G G T T T C atc I I g g gag gag g gag g g g g g g g g g	F CGC R CGT R GAG F CGG F F GAG F F T T T T T T T T T T T T T T T T T	atg M ctg L caa Q gac D gat V cac H gat D	T gac D gag E cgc R ttc F ata I agc S cca P tcc S aag	L cgc R cag Q atg P M agt S ctg L gtt V caa Q aag K ttt	S gtc V gcc A cag Q ttc F ccc T ggc C Cca P ggc	G ctg L cgc R gaa E tcg S tcc S gac D tcc S gag E gat
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V 2651/601 ttg gca aac aat L A N 2741/631 acc acc aag tac T T K Y 2831/661 cac acc tcg tat	tac gg Y A cgt gg R A ttg tc L F tgt cg C Q gac gg D D atg cc M H ccg gg P V cgc ac R I gca tc	L gat p gag gag gag gag gag gag gag gag gag g	Q cga R gaa E cac H gta V cgc R acc T gct A ttc F ctc	tcg s atg M cac H atg W ctg L cag Q aaag K ttg	y gat D cett L gac D caa Q cca P ccc P gtg V gct A ctc	F 2141 2141 2141 2141 2141 2141 2141 2141	D /431 tat /4461 gcc A /491 ata ./521 tcg S ./551 tct S S ./581 tgg W /611 ccg P /641 gtg V /671 aaa	A ttgg W ttgg W act T gtc G G G G G G G G G G G G G G G G G G G	v agt S cac R ggc G tac Y gtg V ccc P ccg	H ggc G tec S aca T cga R ggag E cag Q agc S atg M act	Q tac Y tgg W gca A ttg L gac D ctg L tgg W ggc ttgg t	A tac Y gac D aaaa K ctg L agt S gtg V cac H ttg L	E aca T ggt G acg T aca T cga R G acg D cac H gcc A cca	R tecc S atg M Cac H aaag K acc T ttt F gac T ttt ttg	A cgc R gcc A gta V ccc P acc T tat Y aca T tac Y ggc	G Q 2171/4 2271/4 2271/4 2271/4 2271/4 2271/4 2271/4 2271/4 2271/4 22891/6 22891/6 22891/6 22891/6 22801/6 228	A 141 At case H 171 At case E 171 At case E 1501 At	E aagg gaage E c tac Y S G G G G G T T T C atc I I g g gag gag g gag g g g g g g g g g	F CGC R CGT R GAG F CGG F F GAG F F T T T T T T T T T T T T T T T T T	atg M ctg L caa Q gac D gat V cac H gat D	gac D gag E cgc R ttc F ata I agc S cca P tcc S	L cgc R cag Q atg P M agt S ctg L gtt V caa Q aag K ttt	S gtc V gcc A cag Q ttc F ccc T ggc C Cca P ggc	G ctg L cgc R gaa E tcg S tcc S gac D tcc S gag E gat
2111/421 gac ttt ttc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat L A N N 2741/631 acc acc aag tac T T K Y 2831/661 cac acc tcg tat H T S Y 2921/691 cct cga gag atcc	tac gray A A cgt gar	L gat p gag gag gag gag gag gag gag gag gag g	Q cga R gaa E cac H gta V cgc R acc T gct A ttc F ctc L gtt	tcgs atg M cac H atg W ctg L cag Q aag K ttg L ggt	gat D ctt L gac D caa Q cca P ccc P gtg V gct A ctc L aac	F 2141 a	D /431 Y /441 Y /461 gcc A /491 ata I /521 tcg S /551 tct S /581 tgg W /611 gtg V /671 aaa K (/701 ccc	A tgg W tgg W act T gtc Cgg R gtg Cgg R gtg V ccg R acc N acc	V agt S cac H ggc G tac Y gtg V gag E tgg W ccc P ccg P ttg	H gggc G tecc S aca T cga g E cag Q agc S atg M act T gcc	Q tac Y tag W gca A ttg gac D ctg L tgg W ggc Ctg S ttg	A tac Y gac D aaa K ctg L agt V cac H ttg L tta L	E aca T ggt acg T aca T cga C T cac H gcc A cca P gag	R tec S atg M cac H aag K acc T ttt F gac T ttt ttg L cag	A cgc R gcc A gta V ccc P acc T tat Y aca T tac Y ggc G ggt	G Q 2171/4 2261/4 2261/4 2261/4 261/2 261/4 261/2 261/4 261/2 261/4 261/	A 141 at cas H 171 at cas H 171 at cas E 501 at cas Y 1564 at ct L 171 at cas A 171	E t aag g gaa E c tac Y G G G G G C T C C C C C C C C C C C C C	F Cgc R Cgt R Gag E Cgg P Gag E tttt F atc S gat D	atg M ctg L caa Q gac D gat D gat V cac H gat V	gac D gag E cgc R ttc F ata I . agc S cca P tcc S aag K ctt	Cage R cag Q atg M agt S ctg L gtt V caa Q aag K ttt F act	S gtc V gcc A cag Q ttc P acc T ggc C Cca P ggc C Cag	G ctg L cgc R gaa E tcg S tcc S gac D tcc S gag E gat D gat
2111/421 gac ttt tc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat L A N N 2741/631 acc acc acg tac T T K Y 2831/661 cac acc tcg tat H T S Y 2921/691 cct cga gag atc P R E I	tac gray A A cgt gar	L gat p gag gag gag gag gag gag gag gag gag g	Q cga R gaa E cac H gta V cgc R acc T gct A ttc F ctc L gtt	tcgs atg M cac H atg W ctg L cag Q aag K ttg L ggt	gat D ctt L gac D caa Q cca P ccc P gtg V gct A ctc L aac	F 21411 aaac N 2231 tee S 2321 ggt G 2411 cag Q 2501 gga G 2591 cag R 2681 tee S 2771 cgg R 2951 cgg R 2951	D /431 tat 1	A tgg W tgg W act T gtc Cgg R gtg V ccg R gtg V ccg Aac N acc	V agt S cac H ggc G tac Y gtg V gag E tgg W ccc P ccg P ttg	H gggc G tecc S aca T cga g E cag Q agc S atg M act T gcc	Q tac Y tag W gca A ttg gac D ctg L tgg W ggc Ctg S ttg	A tac Y gac D aaa K ctg L agt V cac H ttg L tta L	E aca T ggt acg T aca T cga C T cac H gcc A cca P gag	R tec S atg M cac H aag K acc T ttt F gac T ttt ttg L cag	A cgc R gcc A gta V ccc P acc T tat Y aca T tac Y ggc G ggt	G Q Q 2171/4 ccc at S I I 22351/5 gtc gtc y Y 2441/5 tcc at S I I 2531/5 gta tcc at S I I 2621/6 gta tcc u C T 2891/6 ccc at L T 2891/6 cca tcc q Y Y L 2891/6 cca tcc tc ctc ctc tc L L L	A 141 at cas H 171	E t aag g gaa E c tac Y G G G G G C T C C C C C C C C C C C C C	F Cgc R Cgt R Gag E Cgg P Gag E tttt F atc S gat D	atg M ctg L caa Q gac D gat D gat V cac H gat V	gac D gag E cgc R ttc F ata I . agc S cca P tcc S aag K ctt	Cage R cag Q atg M agt S ctg L gtt V caa Q aag K ttt F act	S gtc V gcc A cag Q ttc P acc T ggc C Cca P ggc C Cag	G ctg L cgc R gaa E tcg S tcc S gac D tcc S gag E gat D gat
2111/421 gac ttt tc aca D F F T 2201/451 atg cac tat gta H H Y V 2291/481 agg gag ctg tca R E L S 2381/511 gct tta aaa gcc A L K A 2471/541 tac ttt acg ctc Y F T L 2561/571 aag cat gtg gtg K H V V 2651/601 ttg gca aac aat L A N N 2741/631 acc acc acg tac T T K Y 2831/661 cac acc tcg tat H T S Y 2921/691 cct cga gag atc P R E I 3011/721	tac gg Y A cgt gg R A ttg ti L F tgt cc C Q gac gg D D atg cc M H ccg gg P V cgc ai R I gca tc A S tca ti S L	L gat p gag gag gag gag gag gag gag gag gag g	Q cga R gaa E cac H gta V cgc R acc T gct A ttc F ctc L gtt V	tcg s atg M cac H atg W ctg L cag Q aag K ttg L ggt G	y gat D ctt L gac D caa Q cca P ccc P gtg V gct A ctc L aac N	F 21411 aaac N 2231 tee S 2321 ggt G 24111 cag Q 2501 gga C E 2591 cac H 2681 tee S 2771 cgg R R 2861 cgt R 2951 gga G 3041	D /431 Y /461 Y /461 Y /491 Ata I //521 teg S /551 tet S S /551 teg V /611 eeg P V /671 ata Ata Ata Ata Ata Ata Ata Ata Ata Ata	A tgg W tgg W act T gtc V ggt G Cgg R gtg V Ccg R ac T	V agt S cac H ggc G tac Y gtg V ccc P ccg P ttg L	H gggc G tec S aca T cga R gag S aca T cga R gag A gec A	Q tac Y tag W gca A ttg Gac D ctg L tag W ggc ttg F	tac Y gac D aaa K ctg L agt S gtg V cac H ttg L tta L tcg S	E aca ggt G acg T aca T Cga CR	R toc S atg M cac H aag K acc T ttt F gac D acc T ttg Cag Q	A cgc R gcc A gta V ccc P acc T tat Y aca T tac Y ggc G G ggt G	G Q Q 2171/4 con 2171/4 2271/4 2271/4 2771/4	A id1 at tax H id1 id tax H id1	E t aag g gaa c g g g g g g g g g g g g g g g g g g g	F Cgc R Cgt R Gag F E Ccg P Gag E tttt F atc I tcc S Gat I att I	atg M ctg L caa Q gac D gat V cac H gat D gta V cac G gat C	gac D gag E cgc R ttc F ata I . agc S cca P tcc S aag K ctt L	L cgc R cag Q atg M agt V caa Q aag K ttt T act T	S gtc V gcc A cag Q ttc F cec P acc T ggc C cag Q cag Q	G ctg L cgc R gaa E tcg S tcc S gac D tcc S gag E gat D gat D
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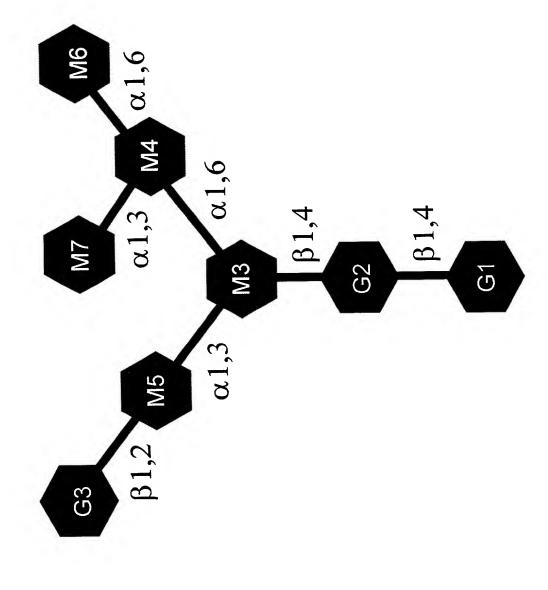
Inventor: ROSE et al. Docket No.: 12243.19USU1 Title: MANNOSIDASE STRUCTURES Serial No.: 09/960226 Sheet 7 of 20

3431/861 3401/851 cet ttg cag gee aac tat tat cee ata cet tet ggt atg tte att gag gat gee aat aeg ega ete aet ete ete aeg ggt caa eeg etg
P L Q A N Y Y P I P S G M F I E D A N T R L T L L T G Q P L
3461/871 3491/881 3521/891 ggt gga tet tet etg gee teg gge gag eta gag att atg caa gat egt ege etg gee age gat gat gaa ege gge etg gga eag ggt gtt
G G S S L A S G E L E I M Q D R R L A S D D E R G L G Q G V
3551/901 3581/911 3611/921 ttg gac aac aag cog gtg ctg cat att tat cgg ctg gtg ctg gag aag gtt aac aac tgt gtc cga cog tca aag ctt cat cct gcc ggc L D N K P V L H I Y R L V L E K V N N C V R P S K L H P A G 3701/951 3671/941 3641/931 tat ttg aca agt gcc gca cac aaa gca tcg cag tca ctg ctg gat cca ctg gac aag ttt ata ttc gct gaa aat gag tgg atc ggg gca
Y L T S A A H K A S Q S L L D P L D K F I F A E N E W I G A
3731/961 3761/971 3791/981 cag ggg caa ttt ggt ggc gat cat cet teg get egt gag gat ete gat gtg teg gtg atg aga ege tta ace aag age teg gee aaa ace Q G Q F G G D H P S A R E D L D V S V M R R L T K S S A K T 3821/991 3851/1001 3881/1011 cag cga gta gge tac gtt ctg cac cgc acc aat ctg atg caa tgc ggc act cca gag gag cat aca cag aag ctg gat gtg tgc cac cta Q R V G Y V L H R T N L M Q C G T P E E H T Q K L D V C H L 3911/1021 3941/1031 3971/1041 ctg ccg aat gtg gcg aga tgc gag cgc acg acg ctg act ttc ctg cag aat ttg gag cac ttg gat ggc atg gtg gcg ccg gaa gtg tgc L P N V A R C E R T T L T F L Q N L E H L D G M V A P E V C 4001/1051 4031/1061 ecc atg gas acc gcc gct tat gtg agc agt cac tca agc TGA METAAYVS SHSS

Inventor: ROSE et al. Docket No.: 12243.19USU1 Title: MANNOSIDASE STRUCTURES Serial No.: 09/960226 Sheet 8 of 20

ALIGNMENT OF EXPRESSED SECRETED DROSPHILA HANNOSIDASE WITH HUMAN MANNOSIDASE Percent SIMILARIY, 52.157 Percent Identity: 43.039 51 LQEKIDHLERILAENNEIISNIEDSVIRLSESVEDDRÄSSGSNFRGAAGS 100 14 DPIRPPLKVÄRSPROGCGÖVVQD VPRVÖNGHLEYDRÄSFRDIDGGYM 62 101 HLL. PSQLEISVDTADCLEASGOSHNSVÄLLYDRÄSFRDIDGGYM 62 101 HLL. PSQLEISVDTADCLEASGOSHNSVÄLLYSFESTRODGYMILS 63 RQCMITKYDELKYNAHTKÄVYVYNYHSUDGHLYFTEKTYDDYHTLES 113 HALMILDNESSKETHERISTYRAFYTHSJÖRDFALKTRUGHTESTYDDYHTLES 1149 RQCHITKÄNDSRAKFHUSISYTARYTHOGENKLUGHESTYKKHOLIEV 115 HALMILDNESSKETHESISTISKHMOLIDIGKKAVKÄLLENGQUETVT 147 116 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAVFÄLLENGQUETVT 147 117 HALMILDNESSKETHESISTISKHMOLIDIGKKAVKÄLLENGQUETVT 147 118 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAVFÄLLENGQUETVT 147 119 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAVFÄLLENGQUETVT 147 124 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAVFÄLLENGGUETVT 147 125 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAVFÄLLENGGUETVT 147 126 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDDFGHSFYT 177 127 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDDFGHSFYT 177 128 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDDFGHSFYT 177 129 RGCHITKÄNDSTAFHTFALLIGGILEGHGALENNGGYRAPRASHÄDDFGHSFYT 177 127 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDDFGHSFYT 177 128 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDDFGHSFYT 177 129 RGCHITKÄNDSTAFHTFALLIGGILEGHGALENNGGYRAPRASHÄDDFGHSFYT 177 120 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDFGHSFYT 177 127 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDFGHSFYT 177 128 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDFGHSFYT 177 129 RGCHITKÄNDSTAFHTFALLIGGILEGHGALENNGGYRAPRASHÄDFGHGFT 177 120 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDFGHGFT 177 127 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDFGHGFT 177 128 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDFGHGT 177 129 OGMVYPDLANSHNYLLLGITEGHGALENNGGYRAPRASHÄDFGHGT 177 120 OGMVYPDLANSHNYLLGITEGHGALENNGGYRAPRASHÄNDFGHGT 177 121 OGMVYPDLANSHNYLLGITEGHGALENNGGYRAPRASHÄNDFGHGT 177 122 OGMVYPDLANSHNYLLGITEGHGANGGYRAPRASHÄNDFGHGT 177 128 OGMVYPDLANSHNYLLGITEGHGANGGYRAPRASHÄNDFGHGT 177 129 OGMVYPDLANSHNY	HANNOSIDASE ELLY: 43.039RSSINHHHUGEP 13 EDGESSGNFEGAGS 100 LELYDRASFRONDGOM 62 [I. LELYDRASFRONDGOM 148 [I. L.		749 KOKLESSVSVOGLESVANOTIMROGARETANIADIOSLOVIELV	APEIRINDIGSLONTEIVA 792	
ALIGNMENT OF EXPRESSED SECRETED PROSPHILA WITH HUMAN MANDGIDASE Percent idented the control of t			749 KGKLESSVSVGLPSVVHQTIMRGG	APERRALVOIGSLONTELVR 792	
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113 MAINLHDNPPERFINAISYFARTHDLOBNIK 119 MAYVIKEDSRKKINSEISYLSKMOIIDIQKI 116 GGWYRDEANSHANNLLQLIEDGUNLKKOFMYI 1248 GGWYRDEANSHANNLLDQLIEDHGMLENNIGY			939 WIGAQQQCODHPSAREDLDVSVMRALIK. SSAKTQRVQVLHRINIMQ 986	SSAKTORVOYVLHRINIMO 986	
163 GOWNPDEANSHMENVLAGLTEGGTMLKGFRAVT 248 GOWNPDEANSHMENVLAGLTEGHEMHENNEGY	KDAVKSLIENGGLEIVT 247		1028 TLELGGEFSPLQSSLPCDIHLVNHZTIGSKVGNGHSNEAALILHRKG.FD 1076	CVGNOHSNEALILHRKG. FD 1076	
248 GGWVMPDEATPHYFALIDQLIEGHQWLENNIGVE	TPTASMAIDPECHEPTH 212		987 C OTPE. EHO. LIDOCHLIN. VANCERTITE/DALEHLOCH 1016 1077 CRFSSKÖTGLFCSTTOGKILVÖRLLINFETVESLIPSSLSLÄHSPPOTONI 1126	VARCERTTLIFLQNLEHLDGM 1026 	
213 PYILOKSGFKNMLIQRIHISVKRELAQUQUEST	248 GGWYNPERYYFRIYFALLDQLLEGHYMLEGHYLVYKROMFALTTEGHYNYK GENETTA 262		1027 VAPEVCPMETAAYVSSHSS 1045		
298 AYLLNRACLSMALIQRUHYAVKKHFALHKTLEFFNRQMADLOSVADILCH	FWRONWDLOSVPDILCH 347	_			
263 MAPPYSYDIPHTGPDPRVCCQFDFKRMGSFQL6CPWKYPPRILEDDAVA 312 348 MAPPYSYDIPHTGPDFKLCQCPDFKLHGGRFQCPWGVPPRILHGGWO 397	SCPWIVEPRIISDONVA 312				
313 ARSDLUDDMKKKELYRINYLLIELODDFRFKQNTBMDVQKVVYBRLEE 362 39 SRAWLDOVKKSKLEFRRYKLAKLANDOPFKSENTBRDLQFRVKSKJESE 447	QNTEMDVORVNYERLFE 362 				
363 HINSONHENYOAGETLOSTEDAVHOAERAGOARE PILSODEFTYA.	. GOAEFPILSODFFTYA 408				
409 DRSDAYASGYYTSRYYHRHÜRVLADIYVRANBHISAMHSND 449	LSAWHSWD 449				
450 GHARIEERLEGARELEFRONDINGTHEN THOUND PORT A 699	VVDYEORNOBALKACOM 499			-	
548 LSSSLYTALTEARKNLGLFQHHDAITGTAKDWVVDYGTRLFHSLAVLEK					
500 VHQQSVYRLLTRPSIVSPDFSFSYFTLDDSRWPGSGVEDSRTTILGEDI 	OSCVEDSRITTILGEDI 549 SQDSLPQKNIIRLSAE. 646				
HARMADON TANANCH TO THE TOTAL TO THE T	LANNEVEACUS PUNSWH 599				
669 HOLLTATHENSTEIN THE	VLTISDSKPEHTSYASN 649				
650 LLENNITELPLOQYPEDVATGDDFRISHAVGNGFTLAFSRQGLIKSIQL 699	GPTLAF SEGGLIKSIQL 699				
733 YYLYKUKUE, DSGIFTIKNMINTEEGITLE, NSFVLLRFDOTGIAKONOM 780	FVLÍRFDOTÓLMKOMM 780 Abbon in Communi 240				
700 TOOSPHYPVHYRFLXXVXSHOUSSGALERGARS VELGGEVUVY 781 KEDGKHHEVNVQESHYGTTIKROKSGAYLELPDGNAKPYVYTTPPFYVVY	GRAFF. VELACEVELYT (40				

Figure 8A





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Figure 8C

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Scrial No.: 12243.19USU1

Trite- MANNOSIDASE STRUCTURES
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The MANNOSIDASE STRUCTURES



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Figure 10A

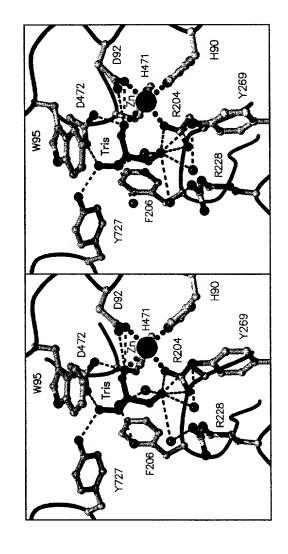


Figure 10B

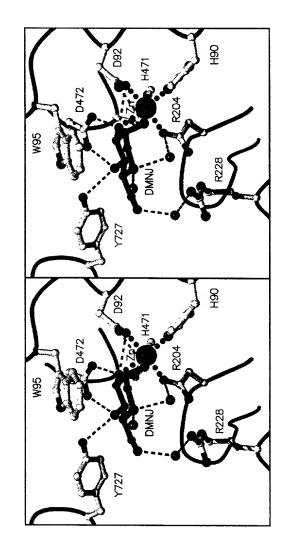
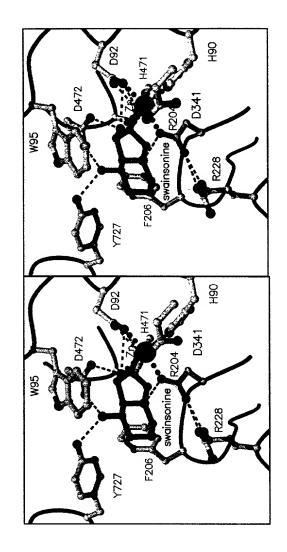
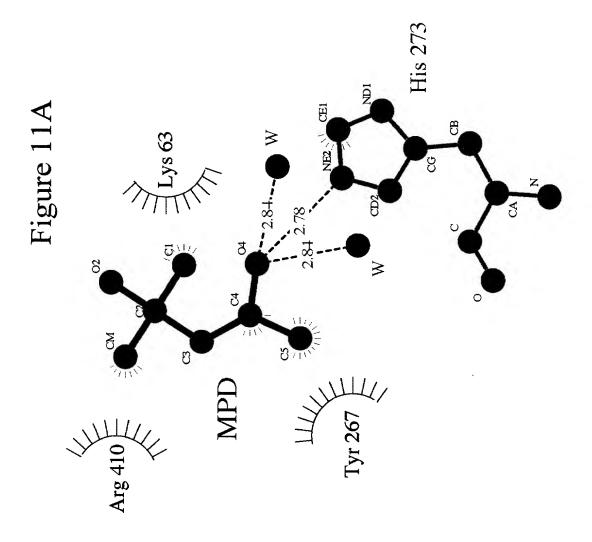


Figure 10C







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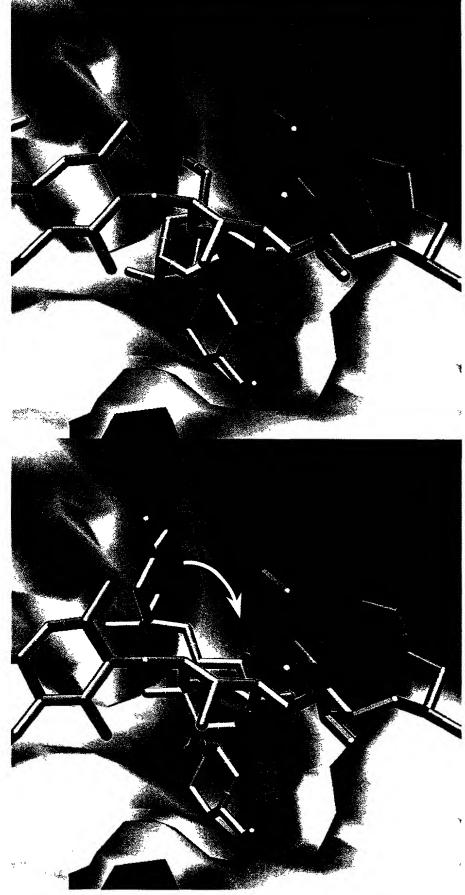


Figure 11C

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